

10/530217

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SEQUENCE LISTING

<110> Nakamura, Yusuke
Katagiri, Toyomasa

<120> GENES AND POLYPEPTIDES RELATING TO HUMAN
MYELOID LEUKEMIA

<130> 082368-003910US

<150> PCT/JP03/09589
<151> 2003-07-29

<150> US 60/414,867
<151> 2002-09-30

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Met Ser
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gag gcc cgc agg gac agc acg agc ctg cag cgc aag aag cca ccc 164
Glu Ala Arg Arg Asp Ser Thr Ser Ser Leu Gln Arg Lys Lys Pro Pro
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tgg cta aag ctg gac att ccc tct gcg gtg ccc ctg acg gca gaa gag 212
Trp Leu Lys Leu Asp Ile Pro Ser Ala Val Pro Leu Thr Ala Glu Glu
20 25 30

ccc agc ttc ctg cag ccc ctg agg cga cag gct ttc ctg agg agt gtg 260
Pro Ser Phe Leu Gln Pro Leu Arg Arg Gln Ala Phe Leu Arg Ser Val
35 40 45 50

agt atg cca gcc gag aca gcc cac atc tct tca ccc cac cat gag ctc 308
Ser Met Pro Ala Glu Thr Ala His Ile Ser Ser Pro His His Glu Leu
55 60 65

cgg cgg ccg gtg ctg caa cgc cag acg tcc atc aca cag acc atc cgc 356
Arg Arg Pro Val Leu Gln Arg Gln Thr Ser Ile Thr Gln Thr Ile Arg
70 75 80

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Lys Leu Lys Pro Gln Val Leu Arg Glu Leu Asp Leu Pro Ser Gln Asp
115 120 125 130

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Asn Val Ser Leu Thr Ser Thr Glu Thr Pro Pro Pro Leu Tyr Val Gly
135 140 145

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Pro Cys Gln Leu Gly Met Gln Lys Ile Ile Asp Pro Leu Ala Arg Gly
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His	Thr	Pro	Val	Thr	Pro	Gly	Ala	Ala	Ser	Leu	Cys	Ser	Phe	Ser	Ser
180						185					190				
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Ser	Arg	Ser	Gly	Phe	His	Arg	Leu	Pro	Arg	Arg	Arg	Lys	Arg	Glu	Ser
195						200					205				210
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gtg	gcc	aag	atg	agc	ttc	cg	gcg	gc	g	ctg	atg	aaa	ggc	cgc	
Val	Ala	Lys	Met	Ser	Phe	Arg	Ala	Ala	Ala	Ala	Leu	Met	Lys	Gly	Arg
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Ser	Val	Arg	Asp	Gly	Thr	Phe	Arg	Arg	Ala	Arg	Arg	Arg	Ser	Phe	Thr
230						235						240			
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cca	gct	agc	ttt	ctg	gag	gag	gac	aca	act	gat	ttc	ccc	gat	gag	ctg
Pro	Ala	Ser	Phe	Leu	Glu	Glu	Asp	Thr	Thr	Asp	Phe	Pro	Asp	Glu	Leu
245						250						255			
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gac	aca	tcc	ttc	ttt	gcc	cg	gaa	gg	atc	ctc	cat	gaa	gag	ctg	tcc
Asp	Thr	Ser	Phe	Phe	Ala	Arg	Glu	Gly	Ile	Leu	His	Glu	Glu	Leu	Ser
260						265					270				
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Thr	Tyr	Pro	Asp	Glu	Val	Phe	Glu	Ser	Pro	Ser	Glu	Ala	Ala	Leu	Lys
275						280					285				290
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gac	tgg	gag	aag	gca	ccg	gag	cag	gcg	gac	ctc	acc	ggc	gg	gcc	ctg
Asp	Trp	Glu	Lys	Ala	Pro	Glu	Gln	Ala	Asp	Leu	Thr	Gly	Gly	Ala	Leu
							295			300			305		
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gac	cgc	agc	gag	ctt	gag	cg	agc	ca	ctg	atg	ctg	ccc	ttg	gag	cga
Asp	Arg	Ser	Glu	Leu	Glu	Arg	Ser	His	Leu	Met	Leu	Pro	Leu	Glu	Arg
310						315						320			
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ggc	tgg	cg	aag	cag	aag	gag	ggc	gc	gca	gc	cc	cag	ccc	aag	gtg
Gly	Trp	Arg	Lys	Gln	Lys	Glu	Gly	Ala	Ala	Ala	Pro	Gln	Pro	Lys	Val
325						330						335			
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cg	ctc	cg	cag	gag	gt	gt	agc	acc	gc	gg	cg	cg	gg	gg	cag
Arg	Leu	Arg	Gln	Glu	Val	Val	Ser	Thr	Ala	Gly	Pro	Arg	Arg	Gly	Gln
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Tyr	Gly	Leu	Gly	Met	Val	Gly	Arg	Leu	Thr	Asn	Arg	Thr	Tyr	Arg	Lys
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Arg	Ile	Asp	Ser	Phe	Val	Lys	Arg	Gln	Ile	Glu	Asp	Met	Asp	Asp	His
390								395					400		
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atc cta gcc gtg tgc atc tat ggc atc gcg ccc gtg ggc ttc tcg cag Ile Leu Ala Val Cys Ile Tyr Gly Ile Ala Pro Val Gly Phe Ser Gln			1412
420	425	430	
cat gag acg gtg gac tcg gtg ctg cgg aac cgc ggg gtc tac gag aac His Glu Thr Val Asp Ser Val Leu Arg Asn Arg Gly Val Tyr Glu Asn			1460
435	440	445	450
gtc aag tac gtg cag cag gag aac ttc tgg atc ggg ccc agc tcg gag Val Lys Tyr Val Gln Gln Glu Asn Phe Trp Ile Gly Pro Ser Ser Glu			1508
455	460	465	
gcc ctc atc cac ctg ggc gcc aag ttt tcg ccc tgc atg cgc cag gac Ala Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys Met Arg Gln Asp			1556
470	475	480	
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485	490	495	
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500	505	510	
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515	520	525	530
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565	570	575	
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595	600	605	610
tcc cgg gag tac tgt gac ttc atg agg ggc tac ttc cat gag gag gcc Ser Arg Glu Tyr Cys Asp Phe Met Arg Gly Tyr Phe His Glu Glu Ala			1988
615	620	625	
acg ctc tgc tct cag gtg cac tgc atg gat gat gtg tgt ggg ctc ctg Thr Leu Cys Ser Gln Val His Cys Met Asp Asp Val Cys Gly Leu Leu			2036
630	635	640	
cct ttt ctc aac ccc gag gtg cct gac cag ttc tac cgc ctg tgg cta Pro Phe Leu Asn Pro Glu Val Pro Asp Gln Phe Tyr Arg Leu Trp Leu			2084
645	650	655	

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Ser Leu Phe Leu His Ala Gly Ile Leu His Cys Leu Val Ser Ile Cys	
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Phe Gln Met Thr Val Leu Arg Asp Leu Glu Lys Leu Ala Gly Trp His	
675 680 685 690	
cgc ata gcc atc atc tac ctg ctg agt ggt gtc acc ggc aac ctg gcc	2228
Arg Ile Ala Ile Ile Tyr Leu Leu Ser Gly Val Thr Gly Asn Leu Ala	
695 700 705	
agt gcc atc ttc ctg cca tac cga gca gag gtg ggt cct gct ggc tcc	2276
Ser Ala Ile Phe Leu Pro Tyr Arg Ala Glu Val Gly Pro Ala Gly Ser	
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Gln Phe Gly Ile Leu Ala Cys Leu Phe Val Glu Leu Phe Gln Ser Trp	
725 730 735	
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Gln Ile Leu Ala Arg Pro Trp Arg Ala Phe Phe Lys Leu Leu Ala Val	
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Val Leu Phe Leu Phe Thr Phe Gly Leu Leu Pro Trp Ile Asp Asn Phe	
755 760 765 770	
gcc cac atc tcg ggg ttc atc agt ggc ctc ttc ctc tcc ttc gcc ttc	2468
Ala His Ile Ser Gly Phe Ile Ser Gly Leu Phe Leu Ser Phe Ala Phe	
775 780 785	
ttg ccc tac atc agc ttt ggc aag ttc gac ctg tac cgg aaa cgc tgc	2516.
Leu Pro Tyr Ile Ser Phe Gly Lys Phe Asp Leu Tyr Arg Lys Arg Cys	
790 795 800	
cag atc atc atc ttt cag gtg gtc ttc ctg ggc ctc ctg gct ggc ctg	2564
Gln Ile Ile Ile Phe Gln Val Val Phe Leu Gly Leu Leu Ala Gly Leu	
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Val Val Leu Phe Tyr Val Tyr Pro Val Arg Cys Glu Trp Cys Glu Phe	
820 825 830	
ctc acc tgc atc ccc ttc act gac aag ttc tgt gag aag tac gaa ctg	2660
Leu Thr Cys Ile Pro Phe Thr Asp Lys Phe Cys Glu Lys Tyr Glu Leu	
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Glu Leu Arg Arg Pro Val Leu Gln Arg Gln Thr Ser Ile Thr Gln Thr
65 70 75 80
Ile Arg Arg Gly Thr Ala Asp Trp Phe Gly Val Ser Lys Asp Ser Asp
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Ser Thr Gln Lys Trp Gln Arg Lys Ser Ile Arg His Cys Ser Gln Arg
100 105 110
Tyr Gly Lys Leu Lys Pro Gln Val Leu Arg Glu Leu Asp Leu Pro Ser
115 120 125
Gln Asp Asn Val Ser Leu Thr Ser Thr Glu Thr Pro Pro Pro Leu Tyr
130 135 140
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Arg Gly Arg Ala Phe Arg Val Ala Asp Asp Thr Ala Glu Gly Leu Ser
165 170 175
Ala Pro His Thr Pro Val Thr Pro Gly Ala Ala Ser Leu Cys Ser Phe
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Ser Ser Ser Arg Ser Gly Phe His Arg Leu Pro Arg Arg Arg Lys Arg
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Glu Ser Val Ala Lys Met Ser Phe Arg Ala Ala Ala Leu Met Lys
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Gly Arg Ser Val Arg Asp Gly Thr Phe Arg Arg Ala Arg Arg Arg Ser
225 230 235 240
Phe Thr Pro Ala Ser Phe Leu Glu Glu Asp Thr Thr Asp Phe Pro Asp
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260 265 270
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275 280 285
Leu Lys Asp Trp Glu Lys Ala Pro Glu Gln Ala Asp Leu Thr Gly Gly
290 295 300
Ala Leu Asp Arg Ser Glu Leu Glu Arg Ser His Leu Met Leu Pro Leu
305 310 315 320
Glu Arg Gly Trp Arg Lys Gln Lys Glu Gly Ala Ala Ala Pro Gln Pro
325 330 335
Lys Val Arg Leu Arg Gln Glu Val Val Ser Thr Ala Gly Pro Arg Arg
340 345 350
Gly Gln Arg Ile Ala Val Pro Val Arg Lys Leu Phe Ala Arg Glu Lys
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Arg Pro Tyr Gly Leu Gly Met Val Gly Arg Leu Thr Asn Arg Thr Tyr
370 375 380
Arg Lys Arg Ile Asp Ser Phe Val Lys Arg Gln Ile Glu Asp Met Asp
385 390 395 400
Asp His Arg Pro Phe Phe Thr Tyr Trp Leu Thr Phe Val His Ser Leu
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Val Thr Ile Leu Ala Val Cys Ile Tyr Gly Ile Ala Pro Val Gly Phe
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Ser Gln His Glu Thr Val Asp Ser Val Leu Arg Asn Arg Gly Val Tyr
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Glu Asn Val Lys Tyr Val Gln Gln Glu Asn Phe Trp Ile Gly His Ser
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 Thr Lys Asn Ser Ala Gly Asn His Thr Asn His Pro His Met Asp Cys
 Val Ile Thr Gly Arg Pro Cys Cys Ile Gly Thr Lys Gly Arg Cys Glu
 Ile Thr Ser Arg Glu Tyr Cys Asp Phe Met Arg Gly Tyr Phe His Glu
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